

PTO/PCT Rec'd 23 JUL 2001

SEQUENCE LISTING

<110> Tsuchiya, Masayuki
Ohtomo, Toshihiko
Sugamata, Yasuhiro
Matsumoto, Kunihiro

<120> Method for screening compounds inhibiting signal
transduction through inflammatory cytokines

<130> 06501-076001

<140> 09/830,144

<141> 2001-04-20

<150> PCT/JP99/05817

<151> 1999-10-21

<150> JP 10/299962

<151> 1998-10-21

<160> 10

<170> PatentIn version 2.0

<210> 1

<211> 2656

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (183)..(1919)

<400> 1

gtcagagatcc attgtgctct aaagacgggt gtggccgctg cctctacccc cgccacggat 60

cgccgggtag taggactgcg cggtccagg ctgagggtcg gtccggaggc ggggtgggcgc 120

gggtctcacc cgattgtcc ggggtggcacc gttcccgcc ccaccgggcg ccgcgaggga 180

tc atg tct aca gcc tct gcc gcc tcc tcc tcc tcc tcc tcc tcc gcc 227

Met Ser Thr Ala Ser Ala Ala Ser Ser Ser Ser Ser Ser Ser Ala

1

5

10

15

ggt gag atg atc gaa gcc cct tcc cag gtc ctc aac ttt gaa gag atc 275

Gly Glu Met Ile Glu Ala Pro Ser Gln Val Leu Asn Phe Glu Glu Ile

20

25

30

gac tac aag gag atc gag gtg gaa gag gtt gtt gga aga gga gcc ttt 323

Asp Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe

35

40

45

gga gtt gtt tgc aaa gct aag tgg aga gca aaa gat gtt gct att aaa 371

Gly Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys

50

55

60

caa ata gaa agt gaa tct gag agg aaa gcg ttt att gta gag ctt cgg	419
Gln Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg	
65 70 75	
cag tta tcc cgt gtg aac cat cct aat att gta aag ctt tat gga gcc	467
Gln Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala	
80 85 90 95	
tgc ttg aat cca gtg tgt ctt gtg atg gaa tat gct gaa ggg ggc tct	515
Cys Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser	
100 105 110	
tta tat aat gtg ctg cat ggt gct gaa cca ttg cca tat tat act gct	563
Leu Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala	
115 120 125	
gcc cac gca atg agt tgg tgt tta cag tgt tcc caa gga gtg gct tat	611
Ala His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr	
130 135 140	
ctt cac agc atg caa ccc aaa gcg cta att cac agg gac ctg aaa cca	659
Leu His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro	
145 150 155	
cca aac tta ctg ctg gtt gca ggg ggg aca gtt cta aaa att tgt gat	707
Pro Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp	
160 165 170 175	
ttt ggt aca gcc tgt gac att cag aca cac atg acc aat aac aag ggg	755
Phe Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly	
180 185 190	
agt gct gct tgg atg gca cct gaa gtt ttt gaa ggt agt aat tac agt	803
Ser Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser	
195 200 205	
gaa aaa tgt gac gtc ttc agc tgg ggt att att ctt tgg gaa gtg ata	851
Glu Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile	
210 215 220	
acg cgt cgg aaa ccc ttt gat gag att ggt ggc cca gct ttc cga atc	899
Thr Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile	
225 230 235	
atg tgg gct gtt cat aat ggt act cga cca cca ctg ata aaa aat tta	947
Met Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu	
240 245 250 255	
cct aag ccc att gag agc ctg atg act cgt tgt tgg tct aaa gat cct	995
Pro Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro	
260 265 270	
tcc cag cgc cct tca atg gag gaa att gtg aaa ata atg act cac ttg	1043
Ser Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu	
275 280 285	

atg cgg tac ttt cca gga gca gat gag cca tta cag tat cct tgt cag	1091
Met Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln	
290 295 300	
tat tca gat gaa gga cag agc aac tct gcc acc agt aca ggc tca ttc	1139
Tyr Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe	
305 310 315	
atg gac att gct tct aca aat acg agt aac aaa agt gac act aat atg	1187
Met Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met	
320 325 330 335	
gag caa gtt cct gcc aca aat gat act att aag cgc tta gaa tca aaa	1235
Glu Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys	
340 345 350	
ttg ttg aaa aat cag gca aag caa cag agt gaa tct gga cgt tta agc	1283
Leu Leu Lys Asn Gln Ala Lys Gln Gln Ser Glu Ser Gly Arg Leu Ser	
355 360 365	
ttg gga gcc tcc cat ggg agc agt gtg gag agc ttg ccc cca acc tct	1331
Leu Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser	
370 375 380	
gag ggc aag agg atg agt gct gac atg tct gaa ata gaa gct agg atc	1379
Glu Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile	
385 390 395	
gcc gca acc aca ggc aac gga cag cca aga cgt aga tcc atc caa gac	1427
Ala Ala Thr Thr Gly Asn Gly Gln Pro Arg Arg Arg Ser Ile Gln Asp	
400 405 410 415	
ttg act gta act gga aca gaa cct ggt cag gtg agc agt agg tca tcc	1475
Leu Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser	
420 425 430	
agt ccc agt gtc aga atg att act acc tca gga cca acc tca gaa aag	1523
Ser Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Thr Glu Lys	
435 440 445	
cca act cga agt cat cca tgg acc cct gat gat tcc aca gat acc aat	1571
Pro Thr Arg Ser His Pro Trp Thr Pro Asp Asp Ser Thr Asp Thr Asn	
450 455 460	
gga tca gat aac tcc atc cca atg gct tat ctt aca ctg gat cac caa	1619
Gly Ser Asp Asn Ser Ile Pro Met Ala Tyr Leu Thr Leu Asp His Gln	
465 470 475	
cta cag cct cta gca ccg tgc cca aac tcc aaa gaa tct atg gca gtg	1667
Leu Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val	
480 485 490 495	
ttt gaa cag cat tgt aaa atg gca caa gaa tat atg aaa gtt caa aca	1715
Phe Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr	
500 505 510	
gaa att gca ttg tta tta cag aga aag caa gaa cta gtt gca gaa ctg	1763

Glu Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu
 515 520 525

gac cag gat gaa aag gac cag caa aat aca tct cgc ctg gta cag gaa 1811
 Asp Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu
 530 535 540

cat aaa aag ctt tta gat gaa aac aaa agc ctt tct act tac tac cag 1859
 His Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln
 545 550 555

caa tgc aaa aaa caa cta gag gtc atc aga agt cag cag cag aaa cga 1907
 Gln Cys Lys Lys Gln Leu Glu Val Ile Arg Ser Gln Gln Gln Lys Arg
 560 565 570 575

caa ggc act tca tgattctctg ggaccggttac attttgaaat atgcaaagaa 1959
 Gln Gly Thr Ser

agactttttt tttaaggaaa ggaaaacctt ataatgaoga ttcattgagt ttagcttttt 2019

ggcgtgttct gaatgccaac tgcctatatatt tgctgcattt ttttcattgt ttattttcct 2079

tttctcatgg tggacataca attttactgt ttcattgcat aacatggtag catctgtgac 2139

ttgaatgagc agcactttgc aacttcaaaa cagatgcagt gaactgtggc tgtatatgca 2199

tgctcattgt gtgaaggcta gcctaacaga acaggaggta tcaaactagc tgctatgtgc 2259

aaacagcgtc cattttttca tattagaggt ggaacctcaa gaatgacttt attottgtat 2319

ctcatctcaa aatattaata atttttttcc caaaagatgg tatataccaa gttaaagaca 2379

gggtattata aatttagagt gattggtggt atattacgga aatacggac ctttagggat 2439

agttccgtgt aagggttttg atgccagcat ccttgatca gtactgaact cagttccatc 2499

cgtaaaatat gtaaaggtaa gtggcagctg ctctatttaa tgaaagcagt tttaccggat 2559

tttgtagac taaaatttga ttgtgataca ttgaacaaaa tggaactcat tttttttaag 2619

gagtaaagat tttctttaga gcacaatgga tctcgac 2656

<210> 2
 <211> 579
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ser Thr Ala Ser Ala Ala Ser Ser Ser Ser Ser Ser Ala Gly
 1 5 10 15

Glu Met Ile Glu Ala Pro Ser Gln Val Leu Asn Phe Glu Glu Ile Asp
 20 25 30

Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe Gly

35	40	45
Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys Gln		
50	55	60
Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg Gln		
65	70	75 80
Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala Cys		
	85	90 95
Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser Leu		
	100	105 110
Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala Ala		
	115	120 125
His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr Leu		
	130	135 140
His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro Pro		
	145	150 155 160
Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp Phe		
	165	170 175
Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly Ser		
	180	185 190
Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser Glu		
	195	200 205
Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile Thr		
	210	215 220
Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile Met		
	225	230 235 240
Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu Pro		
	245	250 255
Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro Ser		
	260	265 270
Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu Met		
	275	280 285
Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln Tyr		
	290	295 300
Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe Met		
	305	310 315 320
Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met Glu		
	325	330 335
Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys Leu		

340							345					350			
Leu	Lys	Asn	Gln	Ala	Lys	Gln	Gln	Ser	Glu	Ser	Gly	Arg	Leu	Ser	Leu
		355					360					365			
Gly	Ala	Ser	His	Gly	Ser	Ser	Val	Glu	Ser	Leu	Pro	Pro	Thr	Ser	Glu
		370				375					380				
Gly	Lys	Arg	Met	Ser	Ala	Asp	Met	Ser	Glu	Ile	Glu	Ala	Arg	Ile	Ala
385					390					395					400
Ala	Thr	Thr	Gly	Asn	Gly	Gln	Pro	Arg	Arg	Arg	Ser	Ile	Gln	Asp	Leu
				405					410					415	
Thr	Val	Thr	Gly	Thr	Glu	Pro	Gly	Gln	Val	Ser	Ser	Arg	Ser	Ser	Ser
			420					425					430		
Pro	Ser	Val	Arg	Met	Ile	Thr	Thr	Ser	Gly	Pro	Thr	Ser	Glu	Lys	Pro
		435					440					445			
Thr	Arg	Ser	His	Pro	Trp	Thr	Pro	Asp	Asp	Ser	Thr	Asp	Thr	Asn	Gly
		450				455					460				
Ser	Asp	Asn	Ser	Ile	Pro	Met	Ala	Tyr	Leu	Thr	Leu	Asp	His	Gln	Leu
465					470					475					480
Gln	Pro	Leu	Ala	Pro	Cys	Pro	Asn	Ser	Lys	Glu	Ser	Met	Ala	Val	Phe
				485					490					495	
Glu	Gln	His	Cys	Lys	Met	Ala	Gln	Glu	Tyr	Met	Lys	Val	Gln	Thr	Glu
			500					505					510		
Ile	Ala	Leu	Leu	Leu	Gln	Arg	Lys	Gln	Glu	Leu	Val	Ala	Glu	Leu	Asp
		515					520					525			
Gln	Asp	Glu	Lys	Asp	Gln	Gln	Asn	Thr	Ser	Arg	Leu	Val	Gln	Glu	His
		530				535					540				
Lys	Lys	Leu	Leu	Asp	Glu	Asn	Lys	Ser	Leu	Ser	Thr	Tyr	Tyr	Gln	Gln
545					550					555					560
Cys	Lys	Lys	Gln	Leu	Glu	Val	Ile	Arg	Ser	Gln	Gln	Gln	Lys	Arg	Gln
				565					570					575	
Gly	Thr	Ser													

```
<210> 3
<211> 1560
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (30)..(1541)
```

<400> 3

gaattcgtgg cccgcagggt tcctccaag atg gcg gcg cag agg agg agc ttg	53
Met Ala Ala Gln Arg Arg Ser Leu	
5	
ctg cag agt gag cag cag cca agc tgg aca gat gac ctg cct ctc tgc	101
Leu Gln Ser Glu Gln Gln Pro Ser Trp Thr Asp Asp Leu Pro Leu Cys	
10 15 20	
cac ctc tct ggg gtt ggc tca gcc tcc aac cgc agc tac tct gct gat	149
His Leu Ser Gly Val Gly Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp	
25 30 35 40	
ggc aag ggc act gag agc cac ccg cca gag gac agc tgg ctc aag ttc	197
Gly Lys Gly Thr Glu Ser His Pro Pro Glu Asp Ser Trp Leu Lys Phe	
45 50 55	
agg agt gag aac aac tgc ttc ctg tat ggg gtc ttc aac ggc tat gat	245
Arg Ser Glu Asn Asn Cys Phe Leu Tyr Gly Val Phe Asn Gly Tyr Asp	
60 65 70	
ggc aac cga gtg acc aac ttc gtg gcc cag cgg ctg tcc gca gag ctc	293
Gly Asn Arg Val Thr Asn Phe Val Ala Gln Arg Leu Ser Ala Glu Leu	
75 80 85	
ctg ctg ggc cag ctg aat gcc gag cac gcc gag gcc gat gtg cgg cgt	341
Leu Leu Gly Gln Leu Asn Ala Glu His Ala Glu Ala Asp Val Arg Arg	
90 95 100	
gtg ctg ctg cag gcc ttc gat gtg gtg gag agg agc ttc ctg gag tcc	389
Val Leu Leu Gln Ala Phe Asp Val Val Glu Arg Ser Phe Leu Glu Ser	
105 110 115 120	
att gac gac gcc ttg gct gag aag gca agc ctc cag tcg caa ttg cca	437
Ile Asp Asp Ala Leu Ala Glu Lys Ala Ser Leu Gln Ser Gln Leu Pro	
125 130 135	
gag gga gtc cct cag cac cag ctg cct cct cag tat cag aag atc ctt	485
Glu Gly Val Pro Gln His Gln Leu Pro Pro Gln Tyr Gln Lys Ile Leu	
140 145 150	
gag aga ctc aag acg tta gag agg gaa att tcg gga ggg gcc atg gcc	533
Glu Arg Leu Lys Thr Leu Glu Arg Glu Ile Ser Gly Gly Ala Met Ala	
155 160 165	
gtt gtg gcg gtc ctt ctc aac aac aag ctc tac gtc gcc aat gtc ggt	581
Val Val Ala Val Leu Leu Asn Asn Lys Leu Tyr Val Ala Asn Val Gly	
170 175 180	
aca aac cgt gca ctt tta tgc aaa tcg aca gtg gat ggg ttg cag gtg	629
Thr Asn Arg Ala Leu Leu Cys Lys Ser Thr Val Asp Gly Leu Gln Val	
185 190 195 200	
aca cag ctg aac gtg gac cac acc aca gag aac gag gat gag ctc ttc	677
Thr Gln Leu Asn Val Asp His Thr Thr Glu Asn Glu Asp Glu Leu Phe	
205 210 215	

cgt ctt tcg cag ctg ggc ttg gat gct gga aag atc aag cag gtg ggg Arg Leu Ser Gln Leu Gly Leu Asp Ala Gly Lys Ile Lys Gln Val Gly 220 225 230	725
atc atc tgt ggg cag gag agc acc cgg cgg atc ggg gat tac aag gtt Ile Ile Cys Gly Gln Glu Ser Thr Arg Arg Ile Gly Asp Tyr Lys Val 235 240 245	773
aaa tat ggc tac acg gac att gac ctt ctc agc gct gcc aag tcc aaa Lys Tyr Gly Tyr Thr Asp Ile Asp Leu Leu Ser Ala Ala Lys Ser Lys 250 255 260	821
cca atc atc gca gag cca gaa atc cat ggg gca cag ccg ctg gat ggg Pro Ile Ile Ala Glu Pro Glu Ile His Gly Ala Gln Pro Leu Asp Gly 265 270 275 280	869
gtg acg ggc ttc ttg gtg ctg atg tcg gag ggg ttg tac aag gcc cta Val Thr Gly Phe Leu Val Leu Met Ser Glu Gly Leu Tyr Lys Ala Leu 285 290 295	917
gag gca gcc cat ggg cct ggg cag gcc aac cag gag att gct gcg atg Glu Ala Ala His Gly Pro Gly Gln Ala Asn Gln Glu Ile Ala Ala Met 300 305 310	965
att gac act gag ttt gcc aag cag acc tcc ctg gac gca gtg gcc cag Ile Asp Thr Glu Phe Ala Lys Gln Thr Ser Leu Asp Ala Val Ala Gln 315 320 325	1013
gcc gtc gtg gac cgg gtg aag cgc atc cac agc gac acc ttc gcc agt Ala Val Val Asp Arg Val Lys Arg Ile His Ser Asp Thr Phe Ala Ser 330 335 340	1061
ggc ggg gag cgt gcc agg ttc tgc ccc cgg cac gag gac atg acc ctg Gly Gly Glu Arg Ala Arg Phe Cys Pro Arg His Glu Asp Met Thr Leu 345 350 355 360	1109
cta gtg agg aac ttt ggc tac ccg ctg ggc gaa atg agc cag ccc aca Leu Val Arg Asn Phe Gly Tyr Pro Leu Gly Glu Met Ser Gln Pro Thr 365 370 375	1157
ccg agc cca gcc cca gct gca gga gga cga gtg tac cct gtg tct gtg Pro Ser Pro Ala Pro Ala Ala Gly Gly Arg Val Tyr Pro Val Ser Val 380 385 390	1205
cca tac tcc agc gcc cag agc acc agc aag acc agc gtg acc ctc tcc Pro Tyr Ser Ser Ala Gln Ser Thr Ser Lys Thr Ser Val Thr Leu Ser 395 400 405	1253
ctt gtc atg ccc tcc cag ggc cag atg gtc aac ggg gct cac agt gct Leu Val Met Pro Ser Gln Gly Gln Met Val Asn Gly Ala His Ser Ala 410 415 420	1301
tcc acc ctg gac gaa gcc acc ccc acc ctc acc aac caa agc ccg acc Ser Thr Leu Asp Glu Ala Thr Pro Thr Leu Thr Asn Gln Ser Pro Thr 425 430 435 440	1349
tta acc ctg cag tcc acc aac acg cac acg cag agc agc agc tcc agc	1397

Leu Thr Leu Gln Ser Thr Asn Thr His Thr Gln Ser Ser Ser Ser Ser
 445 450 455
 tct gac gga ggc ctc ttc cgc tcc cgg ccc gcc cac tcg ctc ccg cct 1445
 Ser Asp Gly Gly Leu Phe Arg Ser Arg Pro Ala His Ser Leu Pro Pro
 460 465 470
 ggc gag gac ggt cgt gtt gag ccc tat gtg gac ttt gct gag ttt tac 1493
 Gly Glu Asp Gly Arg Val Glu Pro Tyr Val Asp Phe Ala Glu Phe Tyr
 475 480 485
 cgc ctc tgg agc gtg gac cat ggc gag cag agc gtg gtg aca gca ccg 1541
 Arg Leu Trp Ser Val Asp His Gly Glu Gln Ser Val Val Thr Ala Pro
 490 495 500
 tagggcagcc ggaggaatg 1560

<210> 4
 <211> 504
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ala Ala Gln Arg Arg Ser Leu Leu Gln Ser Glu Gln Gln Pro Ser
 5 10 15
 Trp Thr Asp Asp Leu Pro Leu Cys His Leu Ser Gly Val Gly Ser Ala
 20 25 30
 Ser Asn Arg Ser Tyr Ser Ala Asp Gly Lys Gly Thr Glu Ser His Pro
 35 40 45
 Pro Glu Asp Ser Trp Leu Lys Phe Arg Ser Glu Asn Asn Cys Phe Leu
 50 55 60
 Tyr Gly Val Phe Asn Gly Tyr Asp Gly Asn Arg Val Thr Asn Phe Val
 65 70 75 80
 Ala Gln Arg Leu Ser Ala Glu Leu Leu Leu Gly Gln Leu Asn Ala Glu
 85 90 95
 His Ala Glu Ala Asp Val Arg Arg Val Leu Leu Gln Ala Phe Asp Val
 100 105 110
 Val Glu Arg Ser Phe Leu Glu Ser Ile Asp Asp Ala Leu Ala Glu Lys
 115 120 125
 Ala Ser Leu Gln Ser Gln Leu Pro Glu Gly Val Pro Gln His Gln Leu
 130 135 140
 Pro Pro Gln Tyr Gln Lys Ile Leu Glu Arg Leu Lys Thr Leu Glu Arg
 145 150 155 160
 Glu Ile Ser Gly Gly Ala Met Ala Val Val Ala Val Leu Leu Asn Asn
 165 170 175

Lys Leu Tyr Val Ala Asn Val Gly Thr Asn Arg Ala Leu Leu Cys Lys
 180 185 190
 Ser Thr Val Asp Gly Leu Gln Val Thr Gln Leu Asn Val Asp His Thr
 195 200 205
 Thr Glu Asn Glu Asp Glu Leu Phe Arg Leu Ser Gln Leu Gly Leu Asp
 210 215 220
 Ala Gly Lys Ile Lys Gln Val Gly Ile Ile Cys Gly Gln Glu Ser Thr
 225 230 235 240
 Arg Arg Ile Gly Asp Tyr Lys Val Lys Tyr Gly Tyr Thr Asp Ile Asp
 245 250 255
 Leu Leu Ser Ala Ala Lys Ser Lys Pro Ile Ile Ala Glu Pro Glu Ile
 260 265 270
 His Gly Ala Gln Pro Leu Asp Gly Val Thr Gly Phe Leu Val Leu Met
 275 280 285
 Ser Glu Gly Leu Tyr Lys Ala Leu Glu Ala Ala His Gly Pro Gly Gln
 290 295 300
 Ala Asn Gln Glu Ile Ala Ala Met Ile Asp Thr Glu Phe Ala Lys Gln
 305 310 315 320
 Thr Ser Leu Asp Ala Val Ala Gln Ala Val Val Asp Arg Val Lys Arg
 325 330 335
 Ile His Ser Asp Thr Phe Ala Ser Gly Gly Glu Arg Ala Arg Phe Cys
 340 345 350
 Pro Arg His Glu Asp Met Thr Leu Leu Val Arg Asn Phe Gly Tyr Pro
 355 360 365
 Leu Gly Glu Met Ser Gln Pro Thr Pro Ser Pro Ala Pro Ala Ala Gly
 370 375 380
 Gly Arg Val Tyr Pro Val Ser Val Pro Tyr Ser Ser Ala Gln Ser Thr
 385 390 395 400
 Ser Lys Thr Ser Val Thr Leu Ser Leu Val Met Pro Ser Gln Gly Gln
 405 410 415
 Met Val Asn Gly Ala His Ser Ala Ser Thr Leu Asp Glu Ala Thr Pro
 420 425 430
 Thr Leu Thr Asn Gln Ser Pro Thr Leu Thr Leu Gln Ser Thr Asn Thr
 435 440 445
 His Thr Gln Ser Ser Ser Ser Ser Ser Asp Gly Gly Leu Phe Arg Ser
 450 455 460
 Arg Pro Ala His Ser Leu Pro Pro Gly Glu Asp Gly Arg Val Glu Pro
 465 470 475 480

Tyr Val Asp Phe Ala Glu Phe Tyr Arg Leu Trp Ser Val Asp His Gly
 485 490 495

Glu Gln Ser Val Val Thr Ala Pro
 500

<210> 5
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence

<400> 5
 ccggaattcc accatggagc ttcggcagtt atcc 34

<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence

<400> 6
 ccggaattcc tactgacaag gatactgt 28

<210> 7
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence

<400> 7
 gtacttcagc acagttttag agaac 25

<210> 8
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificially
 Synthesized Primer Sequence

<400> 8
 ggttgcatgc tgtgaaga 18

<210> 9

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 9
cggaattcga gctccggcag tgcgcg

27

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 10
aactgcaggc tactgacaag gatactgtaa

30